What is claimed is:

1. A method for diagnosing a predisposition to fat deposition in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with fat deposition at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, wherein the PLA2G1B nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:2;

(c) a nucleotide sequence which encodes a polypeptide that is 90% identical to the amino acid sequence of SEQ ID NO:2; and

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic site;

whereby the presence of the polymorphic variation is indicative of a predisposition to fat deposition in the subject.

2. The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. The method of claim 1, wherein the polymorphic variation is a guanine at position 7328 of SEQ ID NO:1.

4. The method of claim 3, wherein the polymorphic variation is in linkage disequilibrium with the guanine at position 7328 of SEQ ID NO:1.

5. The method of claim 1, wherein the polymorphic variation is a thymine at position 9182 of SEQ ID NO:1.

6. The method of claim 5, wherein the polymorphic variation is in linkage disequilibrium with the thymine at position 9182 of SEQ ID NO:1.

7. The method of claim 1, wherein detecting the presence or absence of a polymorphic variation comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to the PLA2G1B nucleotide sequence and hybridizes to a region of the PLA2G1B nucleotide sequence that is adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of the polymorphic variation in the extension products.

8. The method of claim 7, wherein the oligonucleotide is selected from the group consisting of TGAGATGGGAGGATCT (SEQ ID NO: ), ACTGGGAACCTCGA (SEQ ID NO: ), GCTGATGCCGCTG (SEQ ID NO: ), GGAGTGACCCCTT (SEQ ID NO: ), ACACATGACAACTGCTA (SEQ ID NO: ), GGTGTGGGTGTACGG (SEQ ID NO: ), GGTGTGGGTGTACGG (SEQ ID NO: ), CCACACCTATTCATACTC (SEQ ID NO: ), CTTAGGCAGGAGAATC (SEQ ID NO: ), GTAATGCAACTTCAAAC (SEQ ID NO: ); TTAGCATCCTTCAGGCCTAAA (SEQ ID NO: ), GACTCTGCCTCAAAATAAATAAAA (SEQ ID NO: ), GCCGTAGTTGTTGTATTCCAA (SEQ ID NO: ), GTGCAAAACAGTGGGCGATGCT (SEQ ID NO: ), TGATTGCCGAGCCAGAGCA (SEQ ID NO: ), TTTCCATAATAGATATTTATGTAG (SEQ ID NO: ), ATTAGCTGGGCATGGTGGC (SEQ ID NO: ), CACTGTACTCTCCAATAAAGCACC (SEQ ID NO: ), CAAACAAACACACACACAAAAC (SEQ ID NO: ).

9. The method of claim 1, wherein the fat deposition is central fat deposition in the subject.

10. The method of claim 1, wherein the subject is a human.

11. A method for diagnosing a predisposition to leanness in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with leanness at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, wherein the PLA2G1B nucleotide sequence is selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:2;

(c) a nucleotide sequence which encodes a polypeptide that is 90% identical to the amino acid sequence of SEQ ID NO:2; and

(d) a fragment of a nucleotide sequence of (i), (ii), or (iii) comprising the polymorphic site;

whereby the presence of the polymorphic variation is indicative of leanness in the subject.

12. The method of claim 11, wherein the polymorphic variation is an adenine at position 7328 in SEQ ID NO:1.

13. The method of claim 12, wherein the polymorphic variation is in linkage disequilibrium with the adenine at position 7328 of SEQ ID NO:1.

14. The method of claim 11, wherein the polymorphic variation is a guanine at position 9182 of SEQ ID NO:1.

15. The method of claim 14, wherein the polymorphic variation is in linkage disequilibrium with the guanine at position 9182 of SEQ ID NO:1.

16. A method for identifying a polymorphic variation associated with fat deposition proximal to an incident polymorphic variation associated with fat deposition, which comprises:

identifying a polymorphic variant proximal to the incident polymorphic variant associated with fat deposition, wherein the incident polymorphic variant is in a PLA2G1B nucleotide sequence and the PLA2G1B nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence set forth in SEQ ID NO: 1;

(b) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence encoded by a nucleotide sequence set forth as SEQ ID NO: 1; or

(c) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence that is 90% identical to an amino acid sequence encoded by a nucleotide sequence set forth in SEQ ID NO: 1; and

determining the presence or absence of an association of the proximal polymorphic variant with fat deposition.

17. The method of claim 16, wherein the first polymorphic variant is located at position 7328 or 9182 of SEQ ID NO: 1.

18. The method of claim 16, wherein the proximal polymorphic variant is within a region spanning about 5 kb 5' of the incident polymorphic variant and about 5 kb 3' of the incident polymorphic variant.

19. The method of claim 16, which further comprises determining if the proximal polymorphic variant is in linkage disequilibrium with the incident polymorphic variant.

20. The method of claim 16, which further comprises identifying a second polymorphic variant proximal to a proximal polymorphic variant of claim 16 associated with fat deposition and determining if the second polymorphic variant is associated with fat deposition.

21. The method of claim 20, wherein the second proximal polymorphic variant is within a region spanning about 5 kb 5' of the incident polymorphic variant and about 5 kb 3' of the proximal polymorphic variant associated with fat deposition.

22. A method for diagnosing a predisposition to non-insulin dependent diabetes mellitus (NIDDM) in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with NIDDM at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, wherein the PLA2G1B nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:2;

(c) a nucleotide sequence which encodes a polypeptide that is 90% identical to the amino acid sequence of SEQ ID NO:2; and

(d) a fragment of a nucleotide sequence of (i), (ii), or (iii) comprising the polymorphic site;

whereby the presence of the polymorphic variation is indicative of a predisposition to NIDDM in the subject.

23. The method of claim 22, wherein the polymorphic variation is a cytosine at position 7256 of SEQ ID NO:1.

24. The method of claim 23, wherein the polymorphic variation is in linkage disequilibrium with the cytosine at position 7256 of SEQ ID NO:1.

25. A method for identifying a polymorphic variation associated with NIDDM proximal to an incident polymorphic variation associated with NIDDM, which comprises:

identifying a polymorphic variant proximal to the incident polymorphic variant associated with NIDDM, wherein the incident polymorphic variant is in a PLA2G1B nucleotide sequence and the PLA2G1B nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of:

(a) a polynucleotide sequence set forth in SEQ ID NO: 1;

(b) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence encoded by a nucleotide sequence set forth as SEQ ID NO: 1; or

(c) a polynucleotide sequence that encodes a polypeptide having an amino acid sequence that is 90% identical to an amino acid sequence encoded by a nucleotide sequence set forth in SEQ ID NO: 1; and

determining the presence or absence of an association of the proximal polymorphic variant with NIDDM.

26. The method of claim 25, wherein the first polymorphic variant is a cytosine at position 7256 of SEQ ID NO: 1.

27. The method of claim 25, wherein the proximal polymorphic variant is within a region spanning about 5 kb 5' of the incident polymorphic variant and about 5 kb 3' of the incident polymorphic variant.

28. The method of claim 25, which further comprises determining if the proximal polymorphic variant is in linkage disequilibrium with the incident polymorphic variant.

29. The method of claim 25, which further comprises identifying a second polymorphic variant proximal to a proximal polymorphic variant of claim 25 associated with NIDDM and determining if the second polymorphic variant is associated with NIDDM.

30. The method of claim 29, wherein the second proximal polymorphic variant is within a region spanning about 5 kb 5' of the incident polymorphic variant and about 5 kb 3' of the proximal polymorphic variant associated with NIDDM.